The above amendments to the above-captioned application along with the following remarks are being submitted as a full and complete response to the Office Action dated February 15, 2007 (U.S. Patent Office Paper No. 20070203).

Applicants respectfully thank the Examiner for taking time to discuss the formal issues raised in the above-noted Office Action with the Applicants' undersigned representative on May 16, 2007. In view of the above amendments and the following remarks, the Examiner is respectfully requested to give due reconsideration to this application, to indicate the allowability of the claims, and to pass this case to issue.

Status of the Claims

As outlined above, claims 1-17 stand for consideration in this application, wherein claims 1, 5, 9, and 12-16 are being amended to correct formal errors and to more particularly point out and distinctly claim the subject invention.

Additional Amendments

The Specification is being amended to correct formal errors. All amendments to the application are fully supported therein. Applicants hereby submit that no new matter is being introduced into the application through the submission of this response.

Formal Objections

The disclosure was objected to again on the grounds that it contains an embedded hyperlink and/or other form of browser-executable code on page 7, line 3 and page 13, line 9. Also, claims 1 and 14 were objected to on the grounds of informalities. As outlined above, the specification and claims being amended so as to (1) delete the embedded hyperlink; and (2) remove the formal errors identified by the Examiner, respectively.

In addition, Applicants are amending the claims to more particularly point out and distinctly claim the subject invention consistent with the disclosure of the present invention. In particular, the claims are being amended to replace "linked" and "linking" with "connected" and "connecting", respectively. Further, the claims are being amended to clarify the term "degree of relationship" with "degree of association of a relationship" as is fully supported throughout the specification, including but not limited to page 5, lines 1-24; page 11, line 3 to page 12, line 19; and page 17, line 8 to page 18, line 28. Accordingly, withdrawal of the above objections is respectfully requested.

Formal Rejections under 35 U.S.C. §112

The Examiner rejected claims 13-15 under 35 U.S.C. §112, first paragraph, for failing to comply with the enablement requirement. The Examiner rejected claims 1-17 under 35 U.S.C. §112, first paragraph, for failing to comply with the written description requirement. Further, the Examiner rejected claims 1-17·under 35 U.S.C. §112, second paragraph, for being indefinite.

In particular, the Examiner asserted that the term "a lod score" recited in claim 13 and the term "gene clustering" recited in claims 14-15 are not described sufficiently in the Applicants' specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention. Applicants respectfully disagree.

First, the application of a "lod score" to the present invention is illustrated in Figures 11 and 12, and discussed throughout the specification, including page 6, lines 9-14 (*"According to the present invention, for example, when a lod score is obtained by a linkage analysis and a region of genes to be the candidates for the disease gene is determined, the known knowledge can be summarized from it to provide as the disease gene the most reasonable gene or gene group"*); and page 22, line 6 to page 23, line 14 (*"As to the use for the result of linkage analysis, an example that the gene causing idiopathic hypogonadotropic hypogonadism is considered present in chromosome 19p13.2 will be described with reference to Fig. 11 and Fig. 12. The result of linkage analysis is according to JS. Acierno et al., The Journal of Clinical Endocrinology and Metabolism 88(6), pp. 2947-2950, 2003. The analyzed result of q=0.05 is indicated in a solid line in Fig. 11 (for meaning of q, see the linkage analysis in Handbook of statistical genetics, edited by DJ. Balding et al., Wiley, England 2001). A dotted line indicates the score of the network between terms calculated from the co-occurrence relationship of noun phrases in the abstract registered in PUBMED of human 1980-2003 with the query 1 determined as idiopathic hypogonadotropic hypogonadism. As a result, the positions of 0.2-0.4 Mb where they have a peak are presented in step 7 of Fig. 2 (a portion covered by the arrow in Fig. 11) (here, 0.2 Mb was determined as the position of marker rs7815). And, an example of the network of terms in step 8 of Fig. 2 is shown in Fig. 12. In Fig. 12, a second category is the gene name, and the horizontal axis on the screen indicates the gene name (62), showing an example that the first and second queries are displayed in a network form through plural terms on the screen (61). In addition, a lod score is also shown together with a term score on the network display (63), and the lod*

score is shown for each gene on the horizontal axis or together with information on chromosome positions. Here, there is shown an example that a region of 0.2-0.4 Mb which is considered convincing in view of the lod score and text information selected in step 7. The term network having the highest score is indicated in a solid line. The lod score is described in detail by Onda et al., Stroke, 34(7), pp. 1640-1644, 2003"). As noted in Applicants' previous response, the term "lod score" is well known in the art as evidenced in known references, including but not limited to (1) Bioinformatics: "A Practical Guide to the Analysis Genes and Proteins" edited by A.D. Raxevanis and B.F.F. Ouellette 2001 Wiley-Liss, Inc.; (2) Am. J. Hum. Genetics, 66: 1945-1957, 2000; and (3) Proc. National Academy of Science, USA, vol. 95, pp. 14863-14868, December 1998. From such known references, one of skill in the art would know that, in genetics, a "LOD score" is a statistical estimate of whether two loci (the sites of genes) are likely to lie near each other on a chromosome and are therefore likely to be inherited together as a package, wherein LOD stands for logarithm of the odds (to the base 10). A LOD score of three or more is generally taken to indicate that two gene loci are close to each other on the chromosome; a LOD score of three means the odds are a thousand to one in favor of genetic linkage. As cited above, a LOD score is generated and displayed as part of the operation of the present invention.

In view of the knowledge available to one of skill in the art, given the disclosure in the present application regarding the application of a "lod score" to the present invention, all as outlined above, Applicants will contend that one of skill in the art would understand how to make or use the invention. In other words, Applicants will contend that the application of a "lod score" to the present invention, as recited in claim 13, is fully enabled by the disclosure of the present invention.

Second, with respect to the term "gene clustering", the application of a "gene clustering" in the present invention is illustrated in Figures 2 and 13, and discussed throughout the specification, including page 6, lines 15-20 (*"According to the present invention, by displaying the network of terms together with the results of gene/protein clustering of a DNA array and a protein array, the gene/protein configuring the cluster that seems to be noise caused by experiments can be presented"*); page 11, line 3 to page 12, line19 (*"A method of using this system is shown in Fig. 2. A table in which binary relation/multinominal relation manually or automatically extracted from texts and various types of databases and information on its degree of association are accumulated and/or a table in which terms for calculating the co-occurrence and information on its texts are accumulated, and the terms or attributes between the terms are accumulated in the data*

storage system 4 of Fig. 1. The term group query 1 (step 1 of Fig. 2) and query 2 (step 3 of Fig. 2), which are designated by the input part 1 of Fig. 1, are combined under search conditions (an input part 13 of Fig. 1 and step 4 of Fig. 2), and a network of terms coming to have a high score is configured by the CPU system 2 of Fig. 1 and displayed on the display part 3 of Fig. 1 (step 5 of Fig. 2). Among the networks connecting the query 1 and the query 2 depending on a purpose of the user, the network having a degree of association with the highest score is displayed with emphasis (step 6 of Fig. 2). When the experimental results of the linkage analysis and the association study are available, a gene region, which is to be a candidate from the experiment results, is designated under the search conditions of the input part 3 by the input part 1 of Fig. 1 (step 2 of Fig. 2), and the query 2 is automatically specified the gene name of its region (step 3 of Fig. 2). In this case, the query 1 includes a disease name or the disease name and a symptom, but they are not exclusive. Besides, the term network connecting the query 1 and the query 2 is calculated a score and displayed together with a degree of association between each gene and a disease gene of the past information and the lod score of the experimental result to present a candidate gene region (step 7 of Fig. 2). And, specific relationships are clarified by displaying the terms configuring a network with a high score connecting the disease gene and the disease name (step 8 of Fig. 2). To use the array data, the result of clustering from the gene group (to be the query 2) to be the object and the expression information is input in the step 2. Through the same procedure as that described above, a misclustered gene candidate is presented according to the results of clustering using the network of terms for comparison in step 9"); page 23, line 24 to page 25, line 1 ("An example of the term network when data on appearance of a DNA-array is used is shown in Fig. 13. It corresponds to step 9 of Fig. 2. In Fig. 13, an upper section 71 shows a portion linking a gene group used in clustering corresponding to the query 1 and the query 2 by a network of terms. A lower section 72 shows an example of clustering according to the experimental results in which a hierarchical clustering based on expression data of DNA array is shown. The query 1 includes all terms classified into the biological process of gene ontology, and the query 2 describes the network of terms when the gene names clustered are included into the same group by the expression data. In this example, the terms of the query 1 not showing a significant network are not shown (an upper section 71). A hierarchical structure of query 1 terms on the dictionary side of a cell cycle, a DNA replication and a mitotic cell cycle is shown in an upper section 73. According to the experimental data, STE7 belonging to cluster A is different from genes belonging to another A, does not have a network significant with the terms relevant to the cell

cycle but has a network with a response to pheromone. Therefore, it is mis-clustering caused by the experiment noise, and it is suggested that it originally belongs to cluster B. It is preferable that the network and genes that become candidates for the mis-clustering are highlighted because the array data covers a lot of genes. On the other hand, it is suggested that YDR324 is possibly a new gene not having a network with a response to pheromone but related to the response to pheromone without having a significant network with other terms); and page 26, lines 5-11 (*And, it is known that data on the DNA array and protein array contains lots of noises, and it is not easy to perform clustering of genes according to the expression data at high precision. Using this network of terms, a gene to be a misclustering candidate because of a noise can be found easily among genes of which functions are already known*"). Again as noted in Applicants' previous response, the term "gene clustering" is well known in the art as evidenced in known references, including those listed in Applicants' previous response and hereinabove. From such know references, one of skill in the art would understand that the term "gene cluster" means a set of closely related genes that code for the same or similar proteins and which are usually grouped together on the same chromosome.

In view of the knowledge available to one of skill in the art, given the disclosure in the present application regarding the application of "gene clustering" to the present invention, all as outlined above, Applicants will contend that one of skill in the art would understand how to make or use the invention. In other words, Applicants will contend that the application of a "gene clustering" to the present invention, as recited in claims 14-15, is fully enabled by the disclosure of the present invention.

Therefore, Applicants respectfully submit that claims 13-15 comply with the enablement requirement under 35 U.S.C. §112, first paragraph.

Regarding the rejection of claim 1-17 under 35 U.S.C. §112, first paragraph, Applicants will point out that the recitation of "the table including a degree of a relation ship between each two of the terms belonging to the third category" in claims 1 and 16 is supported by Figure 4-7 and their corresponding descriptions in the specification; and the recitation of "a chain of plurality of terms" in claims 1 and 16 is Figures 12 and 13, and their corresponding descriptions.

The recitation of "other external information about said terms" in claim 11 is supported by Figure 12, and its corresponding description in the specification.

The recitation of "a lod score of a result of linkage analysis to said calculation result" in claim 13 is also supported by Figure 12, and its corresponding description in the specification.

The recitations of "gene attributes" and "query is gene with attributes" in claim 14 are supported by Figure 13, and its corresponding description in the specification, including page 23, line 24 to page 25, line 1.

The recitations of "query is genes with attributes" and "similarity of said genes based on the network of terms is inconsistent with a result of said clustering" in claim 15 are also supported by Figure 13, and its corresponding description in the specification, including page 23, line 24 to page 25, line 1.

In view of the above, Applicants will contend that the disclosure of the present invention does provide a written description sufficient to allow one of skill in the art to make or use the invention. Thus, Applicants respectfully submit that claims 1-17 comply with the written description requirement under 35 U.S.C. §112, first paragraph.

With respect to the Examiner's rejection under 35 U.S.C. §112, second paragraph, as outlined above, the claims are being amended in accordance with the Examiner's requirements and to more particularly point out and distinctly claim the subject invention. Thus, Applicants will submit that all the above formal rejections are hereby obviated. Withdrawal of the above-noted rejections is respectfully requested.

Prior Art Rejections

The Examiner rejected claims 1-5, 7-9, 11 and 16-17 under 35 U.S.C. §102(b) as being anticipated by Miller et al. (US Publication No. 2002/0091678). Further, under 35 U.S.C. §103(a), the Examiner rejected claim 10 as being unpatentable over Miller '678 in view of Murray et al. (US Patent No. 6,876,930), and rejected claims 6 and 12-15 as being unpatentable over Miller '678 in view of Chamberlin et al. (US Patent No. 6,941,317). Applicants have reviewed the above-noted rejections, and hereby respectfully traverse.

The present invention as now recited in claim 1 is directed to a network drawing system, comprising: a first input unit designating a first query having terms belonging to a first category; a second input unit designating a second query having terms belonging to a second category; a data storage device storing terms belonging to a third category in a form of a table, the terms of the third category comprising terms from the first category and the second category; a calculation device which calculates a relationship between the input first query and second query through a plurality of terms using the table stored in the data storage device, the table including a degree of association of a relationship between each two of the terms belonging to the third category; and a display device displaying on a screen a network of terms connecting the first query and the second query through a chain of the plurality of

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terms based on a result of calculation made by the calculation device.

Further, the present invention as recited in claim 16 is directed to a network drawing method, comprising the steps of: inputting a first query having terms belonging to a first category into a first input unit; inputting a second query having terms belonging to a second category into a second input unit; using a data storage device storing terms belonging to a third category in a form of a table, the terms of the third category comprising terms from the first category and the second category; calculating a relationship between the input first query and second query through a chain of a plurality of terms by using the table stored in the data storage device, the table including a degree of association of a relationship between each two of the terms belonging to the third category; and displaying on a display device a network of terms connecting the first query and the second query through the plurality of terms according to a result of calculating the relationship.

Miller '678 as cited by the Examiner against the "data storage device" of the present invention only discloses that, when the user selects one of the points 54 or 56, a display of data relating to the object are shown (e.g., the author, frequency tables for occurrence of selected terms in the query, etc.). This reference does not disclose or suggest any structure or operation wherein a data storage device stores terms belonging to a third category in a form of a table, the terms of the third category comprising terms from the first category and the second category and the table including a degree of a relationship between each two of the terms belonging to the third category.

Miller '678 as cited by the Examiner against the "calculation device" of the present invention only discloses that feature vectors have already been calculated for the data objects 38 in the database, or feature vectors for the data objects 38 could be created or modified based on the queries inputted. Further, the relationships between each of the data objects 38 in the database and the query objects are determined. Miller '678 does not disclose or suggest any structure or operation about the relationship between the queries. Moreover, Miller '678 does not teach or suggest any structure or operation for calculating through a plurality of terms using the table stored in the data storage device.

Miller '678 as cited by the Examiner against the "display device" of the present invention only discloses that the plurality points 38 along each query ray are displayed. Miller '678 does not teach or suggest any structure or operation for a network of terms linking the first query and the second query through a chain of plurality of terms based on the result of the calculation.

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As a result of the above, Applicants will contend that Miller '678 falls far short of anticipating each every feature of the present or the combination of features of the present invention as claimed. Thus, the present invention as a whole is distinguishable and thereby allowable over Miller '678.

With respect to the secondary references of Murray '930 and Chamberlin '317, each of these references was cited only for showing additional elements of the present invention, such as those recited in the dependent claims. However, neither reference provides any disclosure, teaching or suggestion that makes up for the deficiencies in Miller '678 such that their combinations could embody all the features of the present invention as now claimed. In other words, even if Miller '678, Murray '930 and Chamberlin '317 were combined, such a combination would still fail to show or suggest each and every feature of the present invention as now claimed, as discussed above. Rather, the present invention as a whole is distinguishable and thereby allowable over all the prior art references cited.
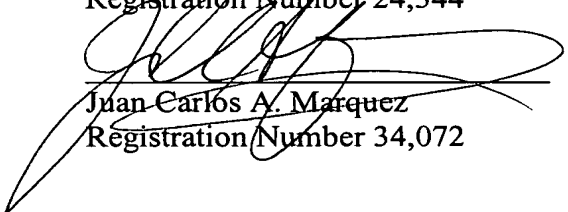
Conclusion

In view of all the above, Applicants respectfully submit that certain clear and distinct differences as discussed exist between the present invention as now claimed and the prior art references upon which the rejections in the Office Action rely. These differences are more than sufficient that the present invention as now claimed would not have been anticipated nor rendered obvious given the prior art. Rather, the present invention as a whole is distinguishable, and thereby allowable over the prior art.

Favorable reconsideration of this application as amended is respectfully solicited. Should there be any outstanding issues requiring discussion that would further the prosecution and allowance of the above-captioned application, the Examiner is invited to contact the Applicants' undersigned representative at the address and phone number indicated below.

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May 18, 2007